



OIPE

## RAW SEQUENCE LISTING

DATE: 06/23/2004

PATENT APPLICATION: US/09/883,839

TIME: 15:46:31

Input Set : A:\600-1-266N SEQLIST.TXT

Output Set: N:\CRF4\06232004\I883839.raw

4 <110> APPLICANT: Kreek, Mary Jeanne  
 5 LaForge, Karl Steven  
 7 <120> TITLE OF INVENTION: Alleles of the Human Mu Opioid Receptor,  
 8 Diagnostic Methods Using Said Alleles, and Methods of  
 9 Treatment Based Thereon  
 11 <130> FILE REFERENCE: 600-1-266N  
 13 <140> CURRENT APPLICATION NUMBER: 09/883,839  
 14 <141> CURRENT FILING DATE: 2001-06-18  
 16 <150> PRIOR APPLICATION NUMBER: 60/212,225  
 17 <151> PRIOR FILING DATE: 2000-06-16  
 19 <160> NUMBER OF SEQ ID NOS: 10  
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 2162  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: misc\_feature  
 30 <222> LOCATION: 2063, 2091  
 31 <223> OTHER INFORMATION: n = A,T,C or G  
 33 <400> SEQUENCE: 1  
 34 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga 60  
 35 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc 120  
 36 ggcgaaagga agcgggtgag gcgcttgga cccgaaaagt ctcggtgctc ctggctacct 180  
 37 cgcacagcgg tgcccgcgg gccgtcagta ccatggacag cagcgtgctc cccacgaacg 240  
 38 ccagcaattg cactgatgcc ttggcgtact caagttgctc cccagcacc agccccggtt 300  
 39 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggt ccgaaccgca 360  
 40 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtccctcc atgatcacgg 420  
 41 ccatcacgat catggccctc tactccatcg tgtgcgtggt ggggctcttc ggaaacttcc 480  
 42 tggtcagtga tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt 540  
 43 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttcag agtgtgaatt 600  
 44 acctaatggg aacatggcca tttggaacca tcctttgcaa gatagtgatc tccatagatt 660  
 45 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg 720  
 46 cagtctgcca cctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca 780  
 47 atgtctgcaa ctggatcctc tcttcagcca ttgggtcttc tgtaatgttc atggctacaa 840  
 48 caaaatacag gcaagggtcc atagattgta cactaacatt ctctcatcca acctggtact 900  
 49 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgctcatca 960  
 50 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcatg ctctctggct 1020  
 51 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctggtg gtggtggctg 1080  
 52 tgttcacgtg ctgctggact ccatttcaca ttacgtcat cattaaagcc ttggttacaa 1140  
 53 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgctcta ggttacacaa 1200  
 54 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca 1260  
 55 gagagtctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc 1320

P.6  
ENTERED

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56 agaacactag agaccacccc tccacggcca atacagtgga tagaactaat catcagctag 1380
57 aaaatctgga agcagaaact gtcctgttgc cctaacaggg tctcatgcca ttccgacctt 1440
58 caccaagctt agaagccacc atgtatgtgg aagcaggttg cttcaagaat gtgtaggagg 1500
59 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca 1560
60 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttgga aggaaaggaa 1620
61 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaccaa acccatcgtg 1680
62 gtatgtgaat tgaagtcac ataaaagggtg acccttctgt ctgtaagatt ttattttcaa 1740
63 gcaaataatt atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca 1800
64 cataaagtaa atgctacctc tgatcaaagc accttgaatg gaaggccga gtctttttag 1860
65 tgtttttgca aggggaatgaa tccattattc tatttttagac ttttaacttc aacttaaaat 1920
66 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa 1980
67 aataacatct ctttcatcta gtcacataat tgcaaggga gagattagca tgaaaggtaa 2040
W--> 68 tctgaaacac agtcatgtgt canctgtaga aagggttgatt ctcatgcact ncaaatactt 2100
69 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtggtttg ttcctggaat 2160
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73 <211> LENGTH: 400
74 <212> TYPE: PRT
75 <213> ORGANISM: Homo sapiens
77 <400> SEQUENCE: 2
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79 1 5 10 15
80 Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
81 20 25 30
82 Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
83 35 40 45
84 Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
85 50 55 60
86 Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
87 65 70 75 80
88 Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
89 85 90 95
90 Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
91 100 105 110
92 Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
93 115 120 125
94 Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
95 130 135 140
96 Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
97 145 150 155 160
98 Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
99 165 170 175
100 Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
101 180 185 190
102 Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
103 195 200 205
104 Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
105 210 215 220
106 His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile

```

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107 225                230                235                240
108 Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
109                245                250                255
110 Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
111                260                265                270
112 Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
113                275                280                285
114 Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
115                290                295                300
116 Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
117 305                310                315                320
118 His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
119                325                330                335
120 Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
121                340                345                350
122 Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
123                355                360                365
124 Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
125                370                375                380
126 Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
127 385                390                395                400
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 2162
132 <212> TYPE: DNA
133 <213> ORGANISM: Homo sapiens
135 <220> FEATURE:
136 <221> NAME/KEY: misc_feature
137 <222> LOCATION: 2063, 2091
138 <223> OTHER INFORMATION: n = A,T,C or G
140 <400> SEQUENCE: 3
141 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga 60
142 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc 120
143 ggcgaaagga agcggctgag gcgcttgaa cccgaaaagt ctcggtgctc ctggctacct 180
144 cgcacagcgg tgcgcgccg gccgtcagta ccattggacag cagcgctgcc ccacgaacg 240
145 ccagcaattg cactgatgcc ttggcgact caagttgccc ccagcacccc agccccgggt 300
146 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggt ccgaaccgca 360
147 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtccctcc atgatcacgg 420
148 ccatcacgat catggccctc tactccatcg tgtgcgtggt ggggctcttc ggaaacttcc 480
149 tggatcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt 540
150 tcaaccttgc tctggcagat gccttagcca ccagtacctt gcccttccag agtgtgaatt 600
151 acctaatggg aacatggcca ttggaacca tcctttgcaa gatagtgatc tccatagatt 660
152 actataacat gttcaccagc atattcacc tctgcaccat gagtggtgat cgatacattg 720
153 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca 780
154 atgtctgcaa ctggatcctc tcttcagcca ttgggtcttc tgtaatgttc atgggtacaa 840
155 caaaatacag gcaaggttcc atagattgta cactaacatt ctctcatcca acctgggtact 900
156 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgctcatca 960
157 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcatg ctctctggct 1020
158 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctggtg gtggtggctg 1080
159 tgttcacgtg ctgctggact cccattcaca ttacgtcat cattaaagcc ttggttacaa 1140

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160 tcccagaaac tacgtttccag actgtttctt ggcacttctg cattgctcta gggttacacaa 1200
161 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca 1260
162 gagagttctg tatcccaacc ttttccaaca ttgagcaaca aaactccact cgaattcgtc 1320
163 agaactactag agaccacccc tccacggcca atacagtggg tagaactaat catcagctag 1380
164 aaaatctgga agcagaaact gctccgttgc cctaacagggg tctcatgcca ttccgacctt 1440
165 caccaagctt agaagccacc atgtatgtgg aagcagggtt cttcaagaat gtgtaggagg 1500
166 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca 1560
167 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttggg aggaaaggaa 1620
168 tataccacac cgaggagtc agtttgtgca agacaccag tggaaaccaa acccatcgtg 1680
169 gtatgtgaat tgaagtcac ataaaagggtg acccttctgt ctgtaagatt ttattttcaa 1740
170 gcaaataatt atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca 1800
171 cataaagtaa atgctacctc tgatcaaagc accttgaatg gaagggtccga gtctttttag 1860
172 tgtttttgca agggaatgaa tccattattc tatttttagac ttttaacttc aacttaaaat 1920
173 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa 1980
174 aataacatct ctttcatcta gctccataat tgcaagggaa gagattagca tgaaaggtaa 2040
W--> 175 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaatactt 2100
176 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtgggttg ttcttggaa 2160
177 tc 2162
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 400
181 <212> TYPE: PRT
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 4
185 Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
186 1 5 10 15
187 Leu Ala Tyr Ser Ser Cys Pro Pro Ala Pro Ser Pro Gly Ser Trp Val
188 20 25 30
189 Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
190 35 40 45
191 Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
192 50 55 60
193 Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
194 65 70 75 80
195 Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
196 85 90 95
197 Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
198 100 105 110
199 Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
200 115 120 125
201 Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
202 130 135 140
203 Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
204 145 150 155 160
205 Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
206 165 170 175
207 Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
208 180 185 190
209 Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
210 195 200 205

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211 Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
212      210                      215                      220
213 His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
214 225                      230                      235                      240
215 Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
216                      245                      250                      255
217 Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
218                      260                      265                      270
219 Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
220                      275                      280                      285
221 Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
222      290                      295                      300
223 Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
224 305                      310                      315                      320
225 His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
226                      325                      330                      335
227 Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
228                      340                      345                      350
229 Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
230                      355                      360                      365
231 Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
232      370                      375                      380
233 Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
234 385                      390                      395                      400

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237 &lt;210&gt; SEQ ID NO: 5

238 &lt;211&gt; LENGTH: 2162

239 &lt;212&gt; TYPE: DNA

240 &lt;213&gt; ORGANISM: Homo sapiens

242 &lt;220&gt; FEATURE:

243 &lt;221&gt; NAME/KEY: misc\_feature

244 &lt;222&gt; LOCATION: 2063, 2091

245 &lt;223&gt; OTHER INFORMATION: n = A,T,C or G

247 &lt;400&gt; SEQUENCE: 5

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248 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga 60
249 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc 120
250 ggcgaaagga agcggctgag gcgcttgga cccgaaaagt ctcggtgctc ctggctacct 180
251 cgcacagcgg tgcccggccc gccgtcagta ccatggacag cagcgtgccc cccacgaacg 240
252 ccagcaattg cactgatgcc ttggcgctact caagttgctc cccagcacc cagcccggtt 300
253 cctgggtcaa cttgtccac ttagatggca acctgaccga cccatgcggt ccgaaccgca 360
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255 ccatcacgat catggccctc tactccatcg tgtgcgtggt ggggctcttc ggaaacttcc 480
256 tggatcatgta tgtgattgtc agataacca agatgaagac tgccaccaac atctacattt 540
257 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttccag agtgtgaatt 600
258 acctaatggg aacatggcca tttggaacca tcctttgcaa gatagtgtc tccatagatt 660
259 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg 720
260 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca 780
261 atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atggctacaa 840
262 caaaatacag gcaaggttcc atagattgta cactaacatt ctctcatcca acctgggtact 900
263 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgctcatca 960

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## RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2063,2091

Seq#:3; N Pos. 2063,2091

Seq#:5; N Pos. 2063,2091

Seq#:7; N Pos. 2063,2091

Seq#:8; N Pos. 2063,2091

Seq#:9; N Pos. 2066,2094

**VERIFICATION SUMMARY**PATENT APPLICATION: **US/09/883,839**

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Input Set : **A:\600-1-266N SEQLIST.TXT**Output Set: **N:\CRF4\06232004\I883839.raw**

L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2040  
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2040  
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2040  
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:2040  
L:438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:2040  
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:2040